

24745-1613

## SEQUENCE LISTING

<110> Edwin L. Madison  
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE  
ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>

<141> Herewith

<150> 60/275,592

<151> 2001-03-13

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3147

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

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<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank #AR081724

<309> 2000-08-31

<310> 5,972,616

<311> 1998-02-20

<312> 1999-10-26

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gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac	148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn	
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Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu	
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gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc	244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe	
60 65 70	
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Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe	

24745-1613

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gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac Ala Leu Lys 125 Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His 130 135				436
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tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag Tyr Trp Ser Glu Phe 160 Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu 155 165 170				532
cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc Arg Val Met Ala 175 Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg 180 185				580
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24745-1613

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Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys	
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gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc	1108
Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro	
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aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg	1156
Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val	
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Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala	
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Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys	
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Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr	
415 420 425	
gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct	1348
Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala	
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Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr	
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Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp	
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gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc	1492
Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala	
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Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu	
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24745-1613

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Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys	
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Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly	
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Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
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Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
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ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
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Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
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agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
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24745-1613

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Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu  
830 835 840

cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccgggg 2599  
Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val  
845 850 855

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Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly  
50 55 60  
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65 70 75 80  
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile  
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100 105 110  
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr  
115 120 125  
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr  
130 135 140  
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser  
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Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu  
165 170 175  
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val  
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Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg  
195 200 205  
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu  
210 215 220  
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala  
225 230 235 240  
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu  
245 250 255  
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly

-6-

24745-1613

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 Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser  
 785                                  790                  795                  800  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly  
                   805                                  810                  815  
 Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln  
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 Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp  
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&lt;211&gt; 3147

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1865)...(2590)

&lt;223&gt; Nucleic acid sequence of protease domain of MTSP1

&lt;400&gt; 3

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1	5	10	15			

24745-1613

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acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg Thr Thr Cys Glu Asn Leu Pro Gln Gln Ile Thr Pro Arg Met Met 160 165 170 175	2389
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gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr 225 230 235	2581
ggg gta tag gggccggggc caccctaatg tgtacacctg cggggccacc Gly Val * 240	2630
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24745-1613

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35     40     45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50     55     60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65     70     75     80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
85     90     95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100    105    110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115    120    125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130    135    140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
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165    170    175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180    185    190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195    200    205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
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Val

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<213> Artificial Sequence

<220>  
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<220>  
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<400> 9  
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<400> 10  
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<210> 11  
<211> 10  
<212> PRT  
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<400> 11  
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24745-1613

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1              5              10

<210> 12
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<212> DNA
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<220>
<223> Primer

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<210> 13
<211> 39
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<220>
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<400> 13
atagcggccg cacactacat accagtcttt gaggcaatc                39

<210> 14
<211> 11
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<400> 14
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<210> 15
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<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (45)...(1361)
<223> MTSP7: full length cDNA

<220>
<221> CDS
<222> (45)...(1361)
<223> MTSP7: full length cDNA

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                                         Met Met Tyr Thr
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cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga                104
Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
5              10              15              20

aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca                152
Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala
                25              30              35

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24745-1613

att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val 40 45 50	200
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 55 60 65	248
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe 70 75 80	296
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg 85 90 95 100	344
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu 105 110 115	392
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg 120 125 130	440
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys 135 140 145	488
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn 150 155 160	536
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn 165 170 175 180	584
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro 185 190 195	632
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr 200 205 210	680
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly 215 220 225	728
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu 230 235 240	776
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile 245 250 255 260	824
gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat	920

24745-1613

Arg	Lys	Ile	Ile	Leu	His	Glu	Asn	Tyr	His	Arg	Glu	Thr	Asn	Glu	Asn		
			280					285					290				
gac	att	gct	ttg	gtt	cag	ctc	tct	act	gga	gtt	gag	ttt	tca	aat	ata	968	
Asp	Ile	Ala	Leu	Val	Gln	Leu	Ser	Thr	Gly	Val	Glu	Phe	Ser	Asn	Ile		
		295					300					305					
gtc	cag	aga	gtt	tgc	ctc	cca	gac	tca	tct	ata	aag	ttg	cca	cct	aaa	1016	
Val	Gln	Arg	Val	Cys	Leu	Pro	Asp	Ser	Ser	Ile	Lys	Leu	Pro	Pro	Lys		
		310				315					320						
aca	agt	gtg	ttc	gtc	aca	gga	ttt	gga	tcc	att	gta	gat	gat	gga	cct	1064	
Thr	Ser	Val	Phe	Val	Thr	Gly	Phe	Gly	Ser	Ile	Val	Asp	Asp	Gly	Pro		
		325			330					335					340		
ata	caa	aat	aca	ctt	cgg	caa	gcc	aga	gtg	gaa	acc	ata	agc	act	gat	1112	
Ile	Gln	Asn	Thr	Leu	Arg	Gln	Ala	Arg	Val	Glu	Thr	Ile	Ser	Thr	Asp		
				345					350					355			
gtg	tgt	aac	aga	aag	gat	gtg	tat	gat	ggc	ctg	ata	act	cca	gga	atg	1160	
Val	Cys	Asn	Arg	Lys	Asp	Val	Tyr	Asp	Gly	Leu	Ile	Thr	Pro	Gly	Met		
			360					365					370				
tta	tgt	gct	gga	ttc	atg	gaa	gga	aaa	ata	gat	gca	tgt	aag	gga	gat	1208	
Leu	Cys	Ala	Gly	Phe	Met	Glu	Gly	Lys	Ile	Asp	Ala	Cys	Lys	Gly	Asp		
		375					380					385					
tct	ggt	gga	cct	ctg	gtt	tat	gat	aat	cat	gac	atc	tggt	tac	att	gta	1256	
Ser	Gly	Gly	Pro	Leu	Val	Tyr	Asp	Asn	His	Asp	Ile	Trp	Tyr	Ile	Val		
		390				395					400						
ggt	ata	gta	agt	tgg	gga	caa	tca	tgt	gca	ctt	ccc	aaa	aaa	cct	gga	1304	
Gly	Ile	Val	Ser	Trp	Gly	Gln	Ser	Cys	Ala	Leu	Pro	Lys	Lys	Pro	Gly		
		405			410				415					420			
gtc	tac	acc	aga	gta	act	aag	tat	cga	gat	tgg	att	gcc	tca	aag	act	1352	
Val	Tyr	Thr	Arg	Val	Thr	Lys	Tyr	Arg	Asp	Trp	Ile	Ala	Ser	Lys	Thr		
				425				430						435			
ggt	atg	tag	tgtggtt	ggt	ccatgag	tta	tacacat	ggc	acacagag	ct						1401	
Gly	Met	*															
gatactcctg	cgtatctt	gtt	attg	tttaaa	ttcatt	tact	ttggatt	tagt	gctttt	gcta	1461						
gatgtcaaga	agcccttc	cag	acccag	acaa	atcta	aatatc	ctgaggt	ggc	ctttac	atac	1521						
gtaggaccaa	accctctc	ta	ccatgag	gga	agaag	acaca	gcaa	atgaca	gacag	cacct	1581						
attccttact	cacaagg	gaa	actgctt	gtg	atactt	cccta	ataag	ataaa	taagt	gggttt	1641						
ccctcaattg	aagacag	gaa	catcatt	tttc	cacagg	atat	gaagag	ctgc	cagta	atgcc	1701						
aaaatccttac	ctcatata	aat	acctgg	agca	tgtgag	attc	ttctag	tgaa	aaaga	acagt	1761						
cttccctgaa	gactcag	ggc	ttcaac	attc	taga	actgat	aaagt	ggacct	tcagt	gtgca	1821						
agaatggaga	agcatgg	gat	ttgcatt	atg	acttga	actg	ggctt	atatc	taata	atata	1881						
gagcactatc	actaac	ctca	acagtt	gaca	ttttaaa	agt	ttttaaa	atgt	atctga	actt	1941						
gctgttaaca	cagtgt	tata	actca	agcac	tagctt	cagg	aagcat	gttg	tggtg	ttaag	2001						
aagcttttct	gatttatt	ct	ttaac	agcat	cttgcc	atct	atatgt	tagt	agcag	ttggc	2061						
ccagaaagga	caaaaaaa		aaaaaa	aaaaaa	aaaaaa	aaaaaa					2100						

<210> 16  
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 <213> Homo sapien

24745-1613

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 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val  
 35 40 45  
 Thr His Phe Val Val Glu Asp Lys Ser Phe Tyr Leu Ala Ser  
 50 55 60  
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser  
 65 70 75 80  
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser  
 85 90 95  
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His  
 100 105 110  
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val  
 115 120 125  
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys  
 130 135 140  
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser  
 145 150 155 160  
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys  
 165 170 175  
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser  
 180 185 190  
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln  
 195 200 205  
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu  
 210 215 220  
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn  
 225 230 235 240  
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro  
 245 250 255  
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val  
 260 265 270  
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu  
 275 280 285  
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu  
 290 295 300  
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys  
 305 310 315 320  
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val  
 325 330 335  
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr  
 340 345 350  
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile  
 355 360 365  
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala  
 370 375 380  
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile  
 385 390 395 400  
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro  
 405 410 415  
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile  
 420 425 430  
 Ala Ser Lys Thr Gly Met  
 435

<210> 17  
 <211> 702  
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&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(702)

&lt;223&gt; Nucleotide sequence encoding Protease Domain

&lt;400&gt; 17

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Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln	
1 5 10 15	
gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc	96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu	
20 25 30	
atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat	144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn	
35 40 45	
aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca	192
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro	
50 55 60	
ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac	240
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr	
65 70 75 80	
cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act	288
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr	
85 90 95	
gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca	336
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser	
100 105 110	
tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga	384
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly	
115 120 125	
tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga	432
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg	
130 135 140	
gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat	480
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp	
145 150 155 160	
ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa	528
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys	
165 170 175	
ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat	576
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn	
180 185 190	
cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt	624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys	
195 200 205	
gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga	672

24745-1613

Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg  
 210 215 220

gat tgg att gcc tca aag act ggt atg tag  
 Asp Trp Ile Ala Ser Lys Thr Gly Met \*  
 225 230

702

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 <212> PRT  
 <213> Homo sapien

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 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu  
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 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn  
 35 40 45  
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro  
 50 55 60  
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr  
 65 70 75 80  
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr  
 85 90 95  
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser  
 100 105 110  
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly  
 115 120 125  
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg  
 130 135 140  
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp  
 145 150 155 160  
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys  
 165 170 175  
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn  
 180 185 190  
 His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys  
 195 200 205  
 Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg  
 210 215 220  
 Asp Trp Ile Ala Ser Lys Thr Gly Met  
 225 230

<210> 19  
 <211> 42  
 <212> DNA  
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<220>  
 <223> Primer

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42

<210> 20  
 <211> 33  
 <212> DNA  
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24745-1613

<220>  
<223> Primer

<400> 20  
agatgagtct gggaggctaa ctctctggac tat 33

<210> 21  
<211> 35  
<212> DNA  
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<220>  
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<400> 21  
attcgcggcc gcctacatac cagtctttga ggcaat 35

<210> 22  
<211> 33  
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<220>  
<223> Primer

<400> 22  
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